

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/538,038A
Source: FWO
Date Processed by STIC: 6/20/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/538,038A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown."
 Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/538,038A

DATE: 06/20/2006
TIME: 15:28:31

Input Set : A:\Sequence Listing.TXT
Output Set: N:\CRF4\06202006\J538038A.raw

2 <110> APPLICANT: Givaudan SA
W--> 3 <120> TITLE OF INVENTION: G-Proteins
W--> 4 <130> FILE REFERENCE: 30069PCT
W--> 5 <140> CURRENT APPLICATION NUMBER: US 10/538,038A
C--> 6 <141> CURRENT FILING DATE: 2005-06-08
7 <150> PRIOR APPLICATION NUMBER: US 60/434,790
8 <151> PRIOR FILING DATE: 2002-12-18
W--> 9 <160> NUMBER OF SEQ ID: 2

ERRORED SEQUENCES

W--> 10 <210> SEQ ID NO: 1
11 <211> LENGTH: 1122 <212> DNA
12 <213> ORGANISM: Homo sapiens
W--> 13 <220> FEATURE:
14 <221> NAME/KEY: CDS
15 <222> LOCATION: (1)..(1122)
16 <223> OTHER INFORMATION:

~~E--> 17 <212> TYPE: ignore this~~

W--> 17 <400> SEQUENCE: 1

18 atggcccgcgt cgctgacctg gcgctgctgc ccctggtgcc tgacggagga tgagaaggcc 60
19 gccgcccggg tggaccagga gatcaacagg atcctcttgg agcagaagaa gcaggaccgc 120
20 ggggagctga agctgctgct tttgggcccc ggcgagagcg ggaagagcac cttcatcaag 180
21 cagatgcgga tcatccacgg cgccggctac tcggaggagg agcgcaaggg cttccggccc 240
22 ctggtctacc agaacatctt cgtgtccatg cgggccatga tcgaggccat ggagcggctg 300
23 cagattccat tcagcaggcc cgagagcaag caccacgcta gcctggtcat gagccaggac 360
24 ccctataaag tgaccacgtt tgagaagcgc tacgtgcgg ccattgcagt gctgtggagg 420
25 gatgccggca tccgggacct ctatgagcgt cggcggaat tccacctgct cgattcagcc 480
26 gtgtactacc tgtccacct ggagcgcat accgaggagg gctacgtccc cacagctcag 540
27 gacgtgctcc gcagccgcat gccaccact ggcataacg agtactgctt ctccgtgcag 600
28 aaaaccaacc tgcggatcgt ggacgtcggg ggccagaagt cagagcgtaa gaaatggatc 660
29 cattgtttcg agaactgat cgccctcatc tacctggcct cactgagtga ataccgaccag 720
30 tgcttgaggg agaacaacca ggagaaccgc atgaaggaga gcctcgcat gtttgggact 780
31 atcctggaac taccctggtt caaaagcaca tccgtcatcc tctttctcaa caaaaccgac 840
32 atcctggagg agaaaatccc cacctccac ctggtacct atttccccag tttccagggc 900
33 cctaagcagg atgctgaggc agccaagagg ttcactctgg acatgtacac gaggatgtac 960
34 accgggtgcg tggacggccc cgagggcagc aacttaaaaa aagaagataa ggaaatctat 1020
35 tctcatatga cctgcgctac tgacacacaa aacgtcaaat tcgtgtttga tgccgtgaca 1080
36 gatataataa taaaagagaa cctcaaagac tgtgggctct tc 1122

38 <210> SEQ ID NO: 2

39 <211> LENGTH: 374

40 <212> TYPE: PRT

DATE: 06/20/2006

TIME: 15:28:31

Input Set : A:\Sequence Listing.TXT

Output Set: N:\CRF4\06202006\J538038A.raw

41 <13> ORGANISM: Homo sapiens
W--> 42 <400> SEQUENCE: 2
43 Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu
E--> 44 5 10 15 15
46 Asp Glu Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu
E--> 47 20 20 25 30
49 Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu
E--> 50 35 40 45
52 Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
E--> 53 50 55 60
55 Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro
E--> 56 65 70 75 80
58 Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala
E--> 59 85 90 95
61 Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His
E--> 62 100 105 110
64 Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu
E--> 65 115 120 125
67 Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile
E--> 68 130 135 140
70 Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala
E--> 71 145 150 155 160
74 Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val
E--> 75 165 170 175
77 Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
E--> 78 180 185 190
80 Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp
E--> 81 195 200 205
83 Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu
E--> 84 210 215 220
86 Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
E--> 87 225 230 235 240
89 Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala
E--> 90 245 250 255
92 Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
E--> 93 260 265 270
95 Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr
E--> 96 275 280 285
98 Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp
E--> 99 290 295 300
101 Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr
E--> 102 305 310 315 320
104 Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Asn Leu Lys Lys Glu Asp
E--> 105 325 330 335
107 Lys Glu Ile Tyr Ser His Met Thr Cys Ala Thr Asp Thr Gln Asn Val
E--> 108 340 345 350
110 Lys Phe Val Phe Asp Ala Val Thr Asp Ile Ile Ile Lys Glu Asn Leu
E--> 111 355 360 365
113 Lys Asp Cys Gly Leu Phe Ser His Leu Ala Thr Tyr Phe Pro Ser

① delete

misaligned

amino acid
number

(see item 3)

on Error

Summary

Sheet 1

Thr
invalid amino acid designator

RAW SEQUENCE LISTING

DATE: 06/20/2006

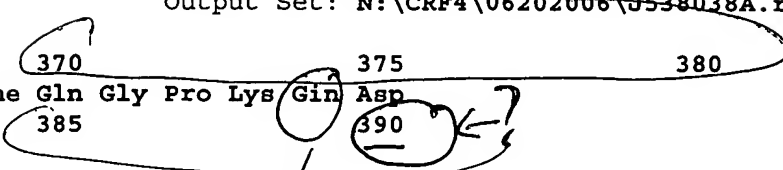
PATENT APPLICATION: US/10/538,038A

TIME: 15:28:31

Input Set : A:\Sequence Listing.TXT

Output Set: N:\CRF4\06202006\J538038A.raw

E--> 114 370 375 380
E--> 116 Phe Gln Gly Pro Lys Gln Asp
E--> 117 385 390



invalid amino acid designator

VERIFICATION SUMMARY

DATE: 06/20/2006

PATENT APPLICATION: US/10/538,038A

TIME: 15:28:32

Input Set : A:\Sequence Listing.TXT

Output Set: N:\CRF4\06202006\J538038A.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:4 M:283 W: Missing Blank Line separator, <130> field identifier
L:5 M:283 W: Missing Blank Line separator, <140> field identifier
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:10 M:283 W: Missing Blank Line separator, <210> field identifier
L:13 M:283 W: Missing Blank Line separator, <220> field identifier
L:17 M:282 E: Numeric Field Identifier Missing, <212> is required.
L:17 M:283 W: Missing Blank Line separator, <400> field identifier
L:17 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:16
L:42 M:283 W: Missing Blank Line separator, <400> field identifier
L:44 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:98 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:116 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1